

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 1, 1999, 15:34:36 ; Search time 1619.02 Seconds
(without alignments)
45.180 Million cell updates/sec

Title: US-09-026-400-5

Perfect score: 23

Sequence: 1 gcnngartggaavtygcnmg 23

Scoring table: IDENTITY_NUC

Searched: 679419 seqs, 1590154680 residues

Database :

GenEmbl.*

- 1: gb_ba1.*
- 2: gb_ba2.*
- 3: gb_cm.*
- 4: gb_ov.*
- 5: gb_pat.*
- 6: gb_ph.*
- 7: gb_pll.*
- 8: gb_pl2.*
- 9: gb_pri.*
- 10: gb_pr2.*
- 11: gb_pr3.*
- 12: gb_ro.*
- 13: gb_st.*
- 14: gb_sts.*
- 15: gb_sy.*
- 16: gb_un.*
- 17: gb_vi.*
- 18: em_fun.*
- 19: em_htg.*
- 20: em_hum1.*
- 21: em_hum2.*
- 22: em_in.*
- 23: em_om.*
- 24: em_or.*
- 25: em_ov.*
- 26: em_pat.*
- 27: em_ph.*
- 28: em_pl.*
- 29: em_ro.*
- 30: em_sts.*
- 31: em_sy.*
- 32: em_un.*
- 33: em_vi.*
- 34: gb_htg1.*
- 35: gb_htg2.*
- 36: gb_in1.*
- 37: gb_in2.*
- 38: em_ba1.*
- 39: em_ba2.*
- 40: em_hum3.*
- 41: em_hum4.*
- 42: gb_pr4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15.8	68.7	205	9 HS164HIR	254791 H.sapiens C

2	15.8	68.7	1721	11	HSU50733	U50733 Human dynam
3	15.8	68.7	25321	36	CEF18E2	275337 Caenorhabdi
4	15.6	67.8	2061	3	BTA6304	AJ006304 Bos tauru
5	15.6	67.8	2716	7	CSLYS4	X93502 S.cerevisia
6	15.6	67.8	30507	7	SC8419	Z49701 S.cerevisia
7	15.6	67.8	2710	8	SCU46154	U46154 Saccharomyc
8	15.6	67.8	4564	10	HSJ6276	AB006276 Homo sapi
9	15.6	67.8	353	10	HSTRPC3GN	X89068 H.sapiens m
10	15.6	67.8	3448	10	HSY13758	Y13758 Homo sapien
11	15.6	67.8	151630	11	AC005154	AC005154 Homo sapi
12	15.6	67.8	147216	11	AF093117	AF093117 Homo sapi
13	15.6	67.8	3417	11	HSU47050	U47050 Human putat
14	15.6	67.8	2842	12	AF057748	AF057748 Mus muscu
15	15.6	67.8	3691	12	AF111107	AF111107 Mus muscu
16	15.6	67.8	3608	12	AF111108	AF111108 Mus muscu
17	15.6	67.8	3340	12	AF136401	AF136401 Rattus no
18	15.6	67.8	3261	12	MMU49069	U49069 Mus musculu
19	15.6	67.8	124156	35	AC006969	AC006969 Homo sapi
20	15.6	67.8	448	35	CETRHOMO	X90598 C.erythroce
21	15.6	67.8	3867	35	CYTRP	Z80230 Calliphora
22	15.6	67.8	86603	37	AC005120	AC005120 Drosophil
23	15.6	67.8	129779	37	AC006214	AC006214 Drosophil
24	15.6	67.8	2796	42	AF080394	AF080394 Homo sapi
25	15.4	67.0	38052	10	HSAC000363	AC000363 Human cos
26	15.4	67.0	76416	11	AC005370	AC005370 Homo sapi
27	15.4	67.0	110000	34	CEY37H9_1	Continuation (2 of
28	15.4	67.0	87805	34	CEY37H9_3	Continuation (4 of
29	15.4	67.0	110000	34	CEY71A12_0	AL021390 Caenorhab
30	15.4	67.0	33455	36	CEW04A8	Z82069 Caenorhab
31	15.2	66.1	2333	1	KPNDAD	L08387 Klebsiella
32	15.2	66.1	37114	1	MSGB38COS	L01095 M. leprae g
33	15.2	66.1	715	4	GGU09261	U09261 Guira guira
34	15.2	66.1	1045	4	SCU37304	U37304 Synthlibora
35	15.2	66.1	1143	4	U892204	U892204 Pharomachru
36	15.2	66.1	71618	7	AB012240	AB012240 Arabidops
37	15.2	66.1	114367	7	ATF10M10	AB035521 Arabidops
38	15.2	66.1	94091	7	ATF28A23	AB012961 Arabidops
39	15.2	66.1	4748	7	PSU51562	U51562 Prunus sero
40	15.2	66.1	6217	9	AB014606	AB014606 Homo sapi
41	15.2	66.1	84170	9	HS130N4	AB014607 Human DNA s
42	15.2	66.1	44888	9	HS130N4B	Z75888 Human DNA s
43	15.2	66.1	288	9	HS44A5F	Z58585 H.sapiens C
44	15.2	66.1	276	9	HS44A5R	Z58586 H.sapiens C
45	15.2	66.1	37738	36	CELF32B5	AF003148 Caenorhab

ALIGNMENTS

RESULT 1

HS164HIR

LOCUS

DEFINITION

ACCESSION

NID

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

COMMENT

HS164HIR 205 bp DNA PRI 17-OCT-1995
H.sapiens CpG island DNA genomic MseI fragment, clone 164hl,
reverse read cpgi64hl.r1a.
254791
g1020832
254791.1 GI:1020832
CpG island; genomic MseI fragment.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 205)
Dodsworth,S.J., Huckle,E., Wilkinson,P. and Micklem,G.
Direct Submission
Submitted (16-OCT-1995) The Sanger Centre, Hinxton, Cambridgeshire,
CB10 1RQ, England. E-mail contact: humquerry@sanger.ac.uk
2 (bases 1 to 205)
Cross,S.H., Charlton,J.A., Nan,X. and Bird,A.P.
Purification of CpG islands using a methylated DNA binding column
Nat. Genet. 6 (3), 236-244 (1994)
Vector: pGEM-5zf(-)

FEATURES	Location/Qualifiers	EMBL:D67647	comes from this gene; cDNA EST yk448f1.3 comes from this gene; cDNA EST yk448f1.5 comes from this gene; cDNA EST yk260g1.3 comes from this gene; cDNA EST yk260g1.5 comes from this gene; cDNA EST yk254d3.5 comes from this gene; cDNA EST yk427e9.5 comes from this gene
source	1. .25321		
	/organism="Caenorhabditis elegans"		
	/db_xref="taxon:6239"		
	/chromosome="v"		
	/clone="F18E2"		
gene	complement(4069. .6129)		
	/gene="F18E2.1"		
CDS	complement(join(4069. .4165,4214. .4473,4519. .4653, 4702. .4812,4962. .5192,5250. .5497,5794. .5937,5988. .6129))		
	/gene="F18E2.1"		
	/note="Similarity to Aspergillus acid phosphatase (NR_0755244)"		
	/codon_start=1		
	/protein_id="CAA99834.1"		
	/db_xref="PID:el345818"		
	/db_xref="PID:g3876094"		
	/db_xref="GI:3876094"		
	/db_xref="SPTREMBL:Q19553"		
	/translation="MSIHITITVLSLVTKICISCTTPDOVHISFTCDTEMAVVNT FSEVQDYYKTKGSGATSTAGSEAWFEGCIRYRHKALIMGLESTEDYDIASR KFSFTLSDPSYKVCVFGDLGIWHGNTSIIKHLGAGDFIVHLGDIADLTIN LGQVDSLVNPEPLISKVPYVIAGNHEDDYQNTYKRFSPDGDHNDGFIYFD NGVHWGVSYTEIYYEYGMQPMVTQYDWLKRDLTANSRAAHPIWTFGRFFY CSDNASCQSFENLVRGLTGLDMPGLPLEFLOTSPVDFGFWGHEHSYERFYPVADRAY VXDNPAYINRPAPVYLISGSAGCTPDALFTDKPWPASARNNDYGSIVTVANRTHI RVEQLSIDKNEQTVDVFWIKDEGHMSGENRRANPCAKTFLQKCHKDVACRSLE INEBL"		
gene	complement(7557. .9729)		
	/gene="F18E2.2"		
CDS	complement(join(7557. .8057,8105. .8669,8825. .9283, 9331. .9642,9698. .9729))		
	/gene="F18E2.2"		
	/note="Similarity to Yeast ATP-dependent transporter (SW:YEM6_YEAST); cDNA EST EMBL:C09155 comes from this gene; cDNA EST yk259a9.3 comes from this gene; cDNA EST yk259a9.5 comes from this gene; cDNA EST yk453c2.3 comes from this gene; cDNA EST yk453c2.5 comes from this gene; cDNA EST yk454c10.5 comes from this gene; cDNA EST yk456g7.3 comes from this gene; cDNA EST yk456g7.5 comes from this gene; cDNA EST yk458h5.3 comes from this gene; cDNA EST yk458h5.5 comes from this gene; cDNA EST yk466h9.3 comes from this gene; cDNA EST yk504g10.3 comes from this gene"		
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	/db_xref="PID:g3876095"		
	/db_xref="GI:3876095"		
	/db_xref="SPTREMBL:Q19554"		
	/translation="WSDAGKKISKEAKKAKAKENYDKTILSMGVGVNLPVEGQOE EHGIGSGALGAFTVSQLSKTQTOLQAMNSMDIKIENFDISAOKLFLDKASLTI VGRYRGLVPGMGKTKTLKHIGAKLAIPSHIDLICYOEIQVDSIDAIDTVKSD KRLALLEEALMEIEDEGTEAAERKEADELDIGADSAPRRARILAGLFSK EMQKPCPTDFSGWRMRISLARALFLEPTLLMLDEPTNHLDNAIWLIDNYLOTWKT LILVSHDQGLSVCTDIILHDNOKLHTYRCNLTLEKKQVQADMVHEKNEQOQOL KAMKEGSAKAEQVQKQANAKKGGKNACKYNDDDAGAPELLQRRKYSYKVF QPPTKLNPVLVGHVNDVFGKDLVFKLNFVDMDSRIAIVPGVNGKSTLLKLL IQKIDPNDGELKRLHRLKRGFDQHANEALNGEPTVFEELCTNFENIDQARKQLGTT GLAAHAHTVKIKDLSGGQKSRVALCNLALGGPDIILDEPTNLDIESIDALAEAIRD FNGGVVMVTHDRLLVVRTDCNLWVNGQIDEIDGDFEDYKKEVLVDALGEALYSKK 10314. .14040		
gene	/gene="F18E2.3"		
CDS	join(10314. .10411,10459. .10866,10920. .11998,12234. .12520, 12568. .13757,13812. .14040)		
	/gene="F18E2.3"		
	/note="cDNA EST EMBL:T00548 comes from this gene; cDNA EST EMBL:D33077 comes from this gene; cDNA EST EMBL:D33596 comes from this gene; cDNA EST EMBL:D35819 comes from this gene; cDNA EST EMBL:D36799 comes from this gene; cDNA EST EMBL:D36456 comes from this gene; cDNA EST EMBL:D72367 comes from this gene; cDNA EST EMBL:D75215 comes from this gene; cDNA EST EMBL:D64592 comes from this gene; cDNA EST		
	/translation="MSTPTDQSPQRMSTRNQARVNTDMAAGNSVEKEPVERSPTE STRGRKRAANDVADLSASFGNLNNESTPPKRRRGGGSLGSRGAFCAPMVRRTTTE ESAYDDRELVAAYKSKKITEAVDSWIGRYNEKFLVATAEMHQEFACGCGKLVTP QMSATLTIKDIICRNTDEEDSADPLVHGSLKRVKRNHNFHTLIIRIKASMLF DSNLMGDFVOLLTGMAQSVQAFRHTATCAKITISALVDVITELLSKSEKTSKQIEA ERAKLNNSAGNEKYEAALVQARTQTEAREEIRQIIGYLFVFRVHYRVDVDPDIRCI CIOELGHMDVYPEHFVSYLKYIGSMDFKVDGVRQRCIRALIPLEFKTLILDKLE LFVNFKDRVLVSMLLDKDLSIETVHLMRVLVFTPLTIKDVVPIVELIYASNRP LAVAAGFLNTKPFSAEKPGKAPTAAINPLVKDLTFTFEGDLHQHATVLDALFES NPVYKDATNGEILLINDOYQDLSNFEFKLIELTCSVQSATGEPVGRHIVKKGAPS AKESRDVEDRQRLETLIELIPLRIKFSDDNEKILNVLNPLHLEQLLEYISARQNT HLMELMGDSLIEKHLEDELLKAVAEIYHLLTNSISALVEGHMKKLLDGVAAEIR KSMQFPDDQSGEEEEALFVSYIKRMAAFGFMDDRDLWDILLKVKVNNYREDTQR DVRSRQCMFLQCFDSFMNKKKEGETPKADQVKRLKRRDQIRIVTITLNEEAGV EQAYLVTCDMLILFGSOLAESKALEPLIWRPDAMVLGNLKFIDVNVDFVSNLSDMD QOEKIEVHKMQHVAQYAKLIIHGAMPVAEASHLIKRYOSHFQDFGDIKNLKSCR EISVYGVMLCEHLTKLYLSQLEDQGTDFLESFNSIRDLAKRLGPAQGVQYAKNRF AISSLHKKAIDFAFEEDYDNHQMNKPIFFLEIAIEFSGKLLAQDKMAVVRVNLKIIYT NRVGTSTVWVEPYRLYLGLSLDRNDDNMSVSRGMTVTSNATMRSTASTRGRGRG RSRIADDF"		
gene	15418. .16931		
	/gene="F18E2.4"		
CDS	join(15418. .15456,15622. .15886,15933. .16028,16166. .16419, 16533. .16931)		
	/gene="F18E2.4"		
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	/protein_id="CAA99837.1"		
	/db_xref="PID:el345821"		
	/db_xref="PID:g3876097"		
	/db_xref="GI:3876097"		
	/db_xref="SPTREMBL:Q19556"		
	/translation="MYTVVSIHRCSLLTIFNMNRITIQVSGVEGIPYVNCSAKTSBEW FATGQRPFLGWSILIFIGVIELLYPTIYMPERKLIHLCTIKIYLCIGVTDMLAIL TCISFGWLFKIGAVYCNPTFYLAGLGLSGMCAQSTLLVLRNVDFVLCRPVS EFLFDGKRVFFSIALITYTGYLVSFMFSPSIFNSAIMAWIADPLTIDPEYKTDITDW YRNHVQTNWNIQFCSTGLYAYCYLVINKMQGKSKASRQVFIQSSICISFTESA MSYNALFTVPAPWVIAELCWSIVHGCPAIIYLTMTKTIETFEFLKFLKLTKNVN NATSFSNNMTSKSNFL"		
gene	join(complement(1233. .1262),complement(816. .909), complement(578. .762),complement(46. .200), complement(275527.1:20448. .20576), complement(275527.1:20263. .20392), complement(275527.1:20063. .20216), complement(275527.1:19840. .19976), complement(275527.1:19578. .19634))		
	/gene="gpa-13"		
CDS	join(complement(1233. .1262),complement(816. .909), complement(578. .762),complement(46. .200), complement(275527.1:20448. .20576), complement(275527.1:20263. .20392), complement(275527.1:20063. .20216), complement(275527.1:19840. .19976), complement(275527.1:19578. .19634))		
	/gene="gpa-13"		
	/note="Similarity to Drosophila Guanine nucleotide-binding protein (SW:GB01_DROME)"		
	Query Match 68.7%; Score 15.8; DB 36; Length 25321; Best Local Similarity 63.6%; Pred. No. 2.2e+02; Matches 14; Conservative 4; Mismatches 4; Indels 0; Gaps 0;		
	QY 1 gcngtngartggaaytygcnm 22		

us-09-026-400-5.rge

Db 3680 GCTGTTGAATTAAGATTTCAC 3659

||||| ||||| ||||| ||||| ||||| :
RESULT 4
LOCUS BTA6304 2061 bp mRNA MAM 11-JUN-1998
DEFINITION Bos taurus mRNA for TRP2 protein.
ACCESSION AJ006304
NID 93152951
KEYWORDS TRP-related; TRP2 gene; Trp2 protein.
SOURCE Bos taurus.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Artiodactylia; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
1 (bases 1 to 2061)
Wissenbach,U.
Direct Submission
Submitted (19-MAY-1998) Wissenbach U., Universitat des Saarlandes,
Pharmakologie und Toxikologie, D-66421 Homburg, Saarland, GERMANY
2 (bases 1 to 2061)
Wissenbach,U., Schroth,G., Philipp,S. and Flockerzi,V.
Structure and mRNA expression of a bovine trp homologue related to
mammalian trp2 transcripts
FEBS Lett. 429 (1), 61-66 (1998)
JOURNAL 98319466 Location/Qualifiers
FEATURES
source
1..2061
/organism="Bos taurus"
/db_xref="taxon:9913"
/tissue_type="testis"
613..1911
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/protein_id="CAA06964.1"
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/translation="MVLSLYLAFTLRLLLAGLAKHCRDPDGAACHYFVSARESE
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ALFAFLGNLVIVPYQETLERLGNFETQFLFTWMGEESHVVDMPQLVPEFVGR
ALGIFITVMIVILLMLMTNSFKIEDADEVKTFARSKLYLSYFREGLITLPVP
FNILSPKAFYLRLVRFRFCCHFCCKTKRPDPIPTFPANPGAGAPGGEGSGSY
RLRVIALVORYIETRQRREERERRDLGNRLTLKTYSRLOSQSVAGVQRAVVEAGP
RRPPGASVLRSYTRVRNSFWNLGPPIPETPELTIPVAIVGVQSSEIGLPDAGAQA
PASGESGPSAPHLVHREQESGADLPQEAADLGAKGT"
BASE COUNT 412 a 604 c 592 g 453 t
ORIGIN

Query Match 67.8%; Score 15.6; DB 3; Length 2061;
Best Local Similarity 65.2%; Pred. No. 3.5e+02;
Matches 15; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 gcngtngartggaayttgcnmq 23
||| ||||| ||||| ||||| :
Db 1192 GACGTGGAGTAGAATTGCAC 1214

RESULT 5
LOCUS CSLYS4/c 2716 bp DNA PLN 28-NOV-1995
DEFINITION S.cerevisiae LYS4 gene.
ACCESSION X93502
NID g1089839
VERSION X93502.1 GI:1089839
KEYWORDS homoacetylase; Lys4 gene.
SOURCE baker's yeast.

ORGANISM Saccharomyces cerevisiae
Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
Saccharomycetaceae; Saccharomyces.
1 (bases 1 to 2716)
Gamonet,F. and Lauquin,J.M.
Unpublished
REFERENCE 2 (bases 1 to 2716)
Gamonet,F.
TITLE Direct Submission
JOURNAL Submitted (27-NOV-1995) F. Gamonet, IBGC-CNRS, CNRS, 1, rue Camille
Saint Saens, F- 33077 Bordeaux Cedex, FRANCE
FEATURES
location/Qualifiers
1..2716
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/strain="GRF88"
/db_xref="taxon:4932"
/chromosome="4"
/clone_lib="CEN-ARS YCP50"
/clone="pv2"
/map="right arm"
/note="isogenic to strain S288-C"
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/gene="lys4"
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277..2358
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/db_xref="PID:g1089840"
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DYVSIKPAHCMSHDNSEVALKEMLGATIKNPQIVTLDHDIONKSNLTKYKN
TENFAKHHDHYPAGRGIGHQIMIESGIAFPLNPVADSHTSYTGLGSLGTPIYR
TDAALWATGOTWQIIPPVAVELQGQLPQVSGKDIIIVLCGLFNNDQVLNHAIFT
GDNLNLPIDHRLTIANNMTTWGALSGLFPVDKTLIDWKRLQKLGINNHPRINPKT
IRALEEKAKIPKADKAHAKKLIIDLATLTHYVSGNVKSNTVQDSOODIKINK
AVLYSCNRSLSQSAADVCCPTGDLNKVKVAPGEVFYVAAASEIEADARKSGAV
EKLKAGCIPISGCGICIGLAGEGLLEPGEVGISATNRFGKRMGSKDALAYLASPV
VAASNVLKISSPAEVLSTSPIPSGVKTEIIEPNVVEEVNAQTETAPKQSVLELEG
PFVSGELVLCADNINTDGIYPKYTYODDPFKKMAQVCMEVDAEFFRTKVPBGDI
PVSFNFGLTSRQEQALLAKGILNVSGSFNFISSRNINNALILTLEIPALIKIL
REKYGAPKELTRTGWFLEKWDVADAKVVVTGSDGDPVILEQKVGLGKLNQLIIVK
GGLPWKVSQI"
277..2358
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/db_xref="SGD:S0002642"
337..2355
/gene="lys4"
/db_xref="SGD:S0002642"
BASE COUNT 814 a 558 c 587 g 757 t
ORIGIN

Query Match 67.8%; Score 15.6; DB 7; Length 2716;
Best Local Similarity 65.2%; Pred. No. 3.4e+02;
Matches 15; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 gcngtngartggaayttgcnmq 23
||| ||||| ||||| ||||| :
Db 1704 GCCGCTGAATGGAATTCGCTG 1682

RESULT 6
LOCUS SC8419/c 30507 bp DNA PLN 11-AUG-1997
DEFINITION S.cerevisiae chromosome IV cosmid 8419.
ACCESSION Z49701 271256

NID	9817819		
VERSION	Z49701.1	GI:817819	
KEYWORDS	AMD; amidase; coatomer; dehydratase; delta element; gluconokinase; PAM1; protein kinase; PRP28; ribosomal protein; SEC26; sigma element; SUP2; transfer RNA-Tyr.		
SOURCE	baker's yeast.		
ORGANISM	Saccharomyces cerevisiae		
REFERENCE	Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.		
AUTHORS	1 (bases 1 to 30507)		
JOURNAL	Oliver,K. and Harris,D.		
REFERENCE	2 (bases 1 to 30507)		
AUTHORS	Barrell,B. and Rajandream,M.A.		
TITLE	Direct Submission		
JOURNAL	Submitted (20-MAY-1995) Saccharomyces cerevisiae chromosome IV sequencing project, Sanger Centre, Hinxton Hall, Hinxton, Cambridge		
COMMENT	CB10 lRQ E-mail: barrell@sanger.ac.uk		
Notes:	All CDS over 100 codons have been analysed. CDS that are completely overlapped and those that are overlapped by more than 50% of their length by a larger CDS have been omitted from this analysis.		
	Details of the omitted CDS are available on request. The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length in codons and the calculated codon adaptation index (CAI) is given for each CDS.		
	Cosmid 8419 is overlapped at the start by cosmid 9934, EMBL id SC9934.		
FEATURES	EMBL accession Z48612 and the end by cosmid 9320.		
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	/chromosome="IV"		
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	/map="4R"		
	<1. 1128		
CDS	/note="YD8419.01, putative dehydratase, incomplete orf - overlaps orf YD934.18, len: > 375, CAI: 0.23, similar to 3-isopropylmalate dehydratase and aconitate dehydratase"		
	/codon_start=1		
	/product="unknown"		
	/protein_id="CAA89720.1"		
	/db_xref="PID:g817820"		
	/db_xref="GI:817820"		
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VERSION	AF093117.1 GI:3687910	
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Eutheria; Primates; Catarrhini; Hominoidea; Homo.		
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Bleischmidt,K., Nordliek,G., Drescher,B., Weber,J., Schattevoy,R.,		
Korenberg,J. and Rosenthal,A.		
Direct Submission		
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JOURNAL	Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany	
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RESULT 13
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DEFINITION Human putative calcium influx channel (htrp3) mRNA, complete cds.
ACCESSION U47050
NID 92295902
VERSION 047050.1 GI:2295902
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3417)
AUTHORS Zhu,X., Jiang,M., Peyton,M., Boulay,G., Hurst,R., Stefani,E. and Birnbaumer,L.
TITLE trp, a novel mammalian gene family essential for agonist-activated capacitative Ca2+ entry
JOURNAL Cell 85 (5), 661-671 (1996)
MEDLINE 96234226
REFERENCE 2 (bases 1 to 3417)
AUTHORS Zhu,X., Peyton,M. and Birnbaumer,L.
TITLE Direct Submission
JOURNAL Submitted (24-JAN-1996) Xi Zhu, Anesthesiology, UCLA School of Medicine, BH-612, CHS, Los Angeles, CA 90095-1778, USA
COMMENT On Aug 4, 1997 this sequence version replaced gi:1326112.
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Best Local Similarity 65.2%; Pred. No. 3.3e+02;
Matches 15; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
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DEFINITION Mus musculus putative capacitative calcium entry channel (Trp6) mRNA, complete cds.
ACCESSION AF057748
NID 93766190
VERSION AF057748.1 GI:3766190
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 2842)
AUTHORS Buess,M., Engler,O., Hirsch,H.H. and Moroni,C.
TITLE Search for oncogenic regulators in an autocrine tumor model using differential display PCR: Identification of novel candidate genes including the calcium channel mtrp 6
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2842)
AUTHORS Buess,M. and Moroni,C.
TITLE Direct Submission
JOURNAL Submitted (07-APR-1998) Institute for Medical Microbiology, Petersplatz 10, Basel 4003, Switzerland
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Fri Oct 1 16:47:13 1999

GenCore version 4.5
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 1, 1999, 15:36:16 ; search time 148.69 Seconds
 (Without alignments)
 38.701 Million cell updates/sec

Title: US-09-026-400-5

Perfect score: 23
Sequence: 1 qcnqtnqartggaayttyqcnmq 23

Scoring table: IDENTITY_NUC

Searched: 311585 seqs, 125096042 residues

Database : N Geneseq 36:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	15.6	67.8	1139	1	V28038	Human transient re	
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7	14.8	64.3	1193	1	V34602	Human uncoupling p	
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9	14.8	64.3	1033	1	V71711	Human uncoupling p	
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C	25	14.2	61.7	1417	1	T73171	Pseudomonas putida
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C	32	14.2	61.7	1401	1	T73167	Pseudomonas putida
C	33	14.2	61.7	237326	1	V57903	Hereditary haemoch
C	34	14.2	61.7	235033	1	V57926	Hereditary haemoch
C	35	14.2	61.7	22080	1	X06751	Salmonella enteric
C	36	14	60.9	1266	1	T89425	Phospholipid scram
C	37	14	60.9	137507	1	V19941	KSHV Long unique c
C	38	14	60.9	35100	1	V73804	KSHV LTR DNA (nucl
C	39	14	60.9	9626	1	X28819	Nucleotide sequenc
C	40	13.6	59.1	855	1	Q20622	C10-16 DNA fragmen
C	41	13.6	59.1	5270	1	Q25387	Rat thyrotropin re
C	42	13.6	59.1	1812	1	Q29419	Nicotiana tabacum
C	43	13.6	59.1	1918	1	Q31539	Lignin peroxidase

ALIGNMENTS

RESULT 1

```

V48147
ID V48147 standard; cDNA to mRNA; 1560 BP.
AC V48147;
DE 27-OCT-1998 (first entry)
DE Nicotianamine aminotransferase 49564.i5 molecular weight protein, gene.
KW ds; nicotianamine aminotransferase; plant; iron absorption;
KW iron deficiency chlorosis.
OS Gramineae sp.
FH Key
FT CDS
FT Location/Qualifiers
FT 62..1447
FT /*tag= a
FT /product= "Nicotianamine aminotransferase"
PN BP-860499-A2.
PN 26-AUG-1998.
PF 19-FEB-1998: 102891.
PR 21-FEB-1997: JP-037499.
PA (SUMO ) SUMITOMO CHEM CO LTD.
PI Mori S, Nakanishi H, Takahashi M;
DR WPI; 98-439341/38.
DR P-PSDB; W61642.
DR New nicotianamine aminotransferase protein and DNA - useful for
PT enhancing iron absorption of plant cells
PS Claim 4; Page 12-13; 17pp; English.
CC The nicotianamine aminotransferase can be used in a plasmid to transform
CC plant cells to produce cells with enhanced iron absorption, and it is
CC implied [though not stated] that plants with improved resistance to iron
CC deficiency chlorosis in calcareous soils can be regenerated from the
CC transformed cells. The gene fragment can be used to detect, amplify
CC and/or isolate Nicotianamine aminotransferase genes.
SQ Sequence 1660 BP; 423 A; 442 C; 430 G; 365 T;

```

```
Query Match      80.0%; Score 18.4; DB 1; Length 1660;
Best Local Similarity 69.6%; Pred. NO. 0.89;
Matches 16; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
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RESULT 2

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V48149
ID V48149 standard; DNA ; 23 BP.
V48149;
AC V48149;
DT 27-OCT-1998 (first entry)
DE Nicotianamine aminotransferase primer 1.
DE ss; nicotianamine aminotransferase; plant; iron absorption; PCR;
KW iron deficiency chlorosis; primer; amplification.
KW Synthetic.
OS Gramineae sp.
OS
FH Key
FT modified_base 3 Location/Qualifiers
FT FT /*tag= a
FT FT /mod_base= I
FT modified_base 6
FT FT /*tag= b
FT FT /mod_base= I
FT modified_base 21
FT FT /*tag= c
FT FT /mod_base= I
EP-860499-A2.
PN 26-AUG-1998.
PD 19-FEB-1998; 102891.
PF 21-FEB-1997; JP-037499.
PR

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Query Match 67.0% Score 15.4; DB 1; Length 11303;
Best Local Similarity 68.4%; Pred. No. 45;
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 4 gngartggaayttgcnm 22
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Db 189 GTCGAATGAATTCGCTA 207

RESULT 7
V54602 ID V54602 standard; cDNA; 1193 BP.
AC V54602; 1998 (first entry)
DT 07-DEC-1998 (first entry)
DE Human uncoupling protein HNF6W60 cDNA.
KW HNF6W60; uncoupling protein; human; body weight disorder; obesity;
KW diabetes; hyperlipidaemia; diagnosis; therapy; vaccine; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 199..1137
FT /tag= a

FT W09839432-AL.
PD 11-SEP-1998.
PD 02-MAR-1998; G00633.
PR 16-JUL-1997; EP-305305.
PR 05-MAR-1997; GB-004551.
PR 18-MAR-1997; GB-005614.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PI Beekley LJ, Godden RJ, Paine K;
DR WPI; 98-495841/42.
DR P-PSDB; W68197.
PT New isolated human uncoupling polypeptide(s) - used to develop
PT products for the diagnosis, prevention and treatment of body weight
PT disorders, obesity and diabetes
PT Claim 3; Page 24-25; 41pp; English.
PS This isolated polynucleotide (PN) codes for novel human uncoupling
CC protein HNF6W60 (see W68197). HNF6W60 polynucleotides (see also
CC V54603-04) can be obtained from a cDNA library derived from mRNA in
CC cells of human brain frontal cortex, rhabdomyosarcoma, foetal heart
CC and skeletal muscle using expressed sequence tag analysis. The
CC invention relates to HNF6W60 polypeptides and recombinant materials
CC and methods for their production. It also relates to methods for
CC using such HNF6W60 polypeptides and polynucleotides. Such uses
CC include the treatment of obesity, diabetes, hyperlipidaemia and
CC body weight disorders. The invention also provides methods to
CC identify agonists and antagonists, and methods for treating
CC conditions associated with HNF6W60 imbalance for the identified
CC compounds. In addition, diagnostic assays for detecting diseases
CC associated with inappropriate HNF6W60 activity or levels are
CC provided.
SQ Sequence 1193 BP; 252 A; 370 C; 343 G; 228 T;

Query Match 64.3% Score 14.8; DB 1; Length 1193;
Best Local Similarity 61.9%; Pred. No. 66;
Matches 13; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 cngtngartggaayttgcnm 22
|||:||||:||||:|

Db 730 CTCTGGGAAGAACITTCGCC 750

RESULT 8
V71710 ID V71710 standard; DNA; 1220 BP.
AC V71710;
DT 09-FEB-1999 (first entry)
DE Human uncoupling protein 3 (UCP3) encoding DNA.
KW Uncoupling protein 3; UCP3; thermogenesis; mammal; enhancer; drug;
KW protein catabolism; anti-obesity; inhibitor; muscle wasting; infection;
KW HIV; cancer; tumour cachexia; muscle disease; muscular dystrophy;

[illegible]

PN W09850542-A1.
 PD 12-NOV-1998.
 PF 05-MAY-1998; E02645.
 PR 07-MAY-1997; CH-001072.
 PA (NOVS) NOVARTIS AG.
 PI Boss O, Giacobino J, Muzzin P;
 DR WPI: 98-610382/51.
 DR P-PSDB: W83379.
 PT New human skeletal muscle uncoupling proteins UCP3L and UCP3S -
 PT useful for controlling thermogenesis in human skeletal muscle and
 PT heart, e.g. for treating obesity and cachexia
 PS Claim 1; Page 14-15; 26pp; English.
 CC The present sequence encodes human uncoupling protein UCP3L. UCP3
 CC uncouples oxidative phosphorylation and synthesis of adenosine
 CC triphosphate in the mitochondria of skeletal muscle. The coding
 CC sequences for UCP3L and UCP3S are useful for gene therapy of
 CC dysfunctions of thermogenesis in human skeletal muscle and heart which
 CC result from a lack of UCP3 and which can induce disorders such as
 CC obesity or cachexia. Antisense oligonucleotides to UCP3L and UCP3S can
 CC be used for correcting an excess of UCP3. Modification of endogenous
 CC UCP3 activity (using activators or inhibitors of UCP3) is used to induce
 CC bodyweight loss (loss of adipose mass and maintenance of the lean mass)
 CC in all types of obesity by promoting the dissipation of energy; for
 CC preventing an excessive weight regain following restrictive food diet or
 CC type II diabetes by improving sensitivity to insulin; for preventing
 CC hypertension; for increasing muscle mass in states of cachexia; for
 CC treatment of insufficiencies or disturbances of cardiac rhythm due to a
 CC dysfunction of UCP3; and for the treatment of neuromuscular diseases due
 CC to a dysfunction of UCP3. The uncoupling proteins can also be used to
 CC raise antibodies, e.g. for diagnosis. Knowledge of the UCP3 genes allows
 CC generation of transgenic animals, e.g. for screening substances which
 CC modify UCP3 expression or activity or for investigating the biological
 CC role of UCP3.
 SQ Sequence 1231 BP; 271 A; 371 C; 345 G; 244 T;
 Query Match 64.3%; Score 14.8; DB 1; Length 1231;
 Best Local Similarity 61.9%; Pred. No. 66;
 Matches 13; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
 QY 2 cngtngartggaayttgcnm 22
 | | | | | : | | | | | : | | :
 Db 685 CTGTGGAAGGAACCTTGCC 705
 RESULT 11
 V72691
 ID V72691 standard; cDNA; 1132 BP.
 AC V72691;
 DT 22-FEB-1999 (first entry)
 DE Human uncoupling protein UCP3S encoding cDNA.
 KW Human; uncoupling protein; UCP3L; UCP3S; oxidative phosphorylation;
 KW adenosine triphosphate; mitochondria; skeletal muscle; gene therapy;
 KW thermogenesis; heart; obesity; cachexia; type II diabetes; hypertension;
 KW insulin sensitivity; neuromuscular disease; ss.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT CDS 154..991
 FT /*tag= a
 FT /*product= "UCP3S"
 PN W09850542-A1.
 PD 12-NOV-1998.
 PF 05-MAY-1998; E02645.
 PR 07-MAY-1997; CH-001072.
 PA (NOVS) NOVARTIS AG.
 PI Boss O, Giacobino J, Muzzin P;
 DR WPI: 98-610382/51.
 DR P-PSDB: W83380.
 PT New human skeletal muscle uncoupling proteins UCP3L and UCP3S -
 PT useful for controlling thermogenesis in human skeletal muscle and

PT heart, e.g. for treating obesity and cachexia
 PS Claim 3; Page 17-18; 26pp; English.
 CC The present sequence encodes human uncoupling protein UCP3S. UCP3
 CC uncouples oxidative phosphorylation and synthesis of adenosine
 CC triphosphate in the mitochondria of skeletal muscle. The coding
 CC sequences for UCP3L and UCP3S are useful for gene therapy of
 CC dysfunctions of thermogenesis in human skeletal muscle and heart which
 CC result from a lack of UCP3 and which can induce disorders such as
 CC obesity or cachexia. Antisense oligonucleotides to UCP3L and UCP3S can
 CC be used for correcting an excess of UCP3. Modification of endogenous
 CC UCP3 activity (using activators or inhibitors of UCP3) is used to induce
 CC bodyweight loss (loss of adipose mass and maintenance of the lean mass)
 CC in all types of obesity by promoting the dissipation of energy; for
 CC preventing an excessive weight regain following restrictive food diet or
 CC type II diabetes by improving sensitivity to insulin; for preventing
 CC hypertension; for increasing muscle mass in states of cachexia; for
 CC treatment of insufficiencies or disturbances of cardiac rhythm due to a
 CC dysfunction of UCP3; and for the treatment of neuromuscular diseases due
 CC to a dysfunction of UCP3. The uncoupling proteins can also be used to
 CC raise antibodies, e.g. for diagnosis. Knowledge of the UCP3 genes allows
 CC generation of transgenic animals, e.g. for screening substances which
 CC modify UCP3 expression or activity or for investigating the biological
 CC role of UCP3.
 SQ Sequence 1132 BP; 245 A; 351 C; 321 G; 215 T;
 Query Match 64.3%; Score 14.8; DB 1; Length 1132;
 Best Local Similarity 61.9%; Pred. No. 65;
 Matches 13; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
 QY 2 cngtngartggaayttgcnm 22
 | | | | | : | | | | | : | | :
 Db 685 CTGTGGAAGGAACCTTGCC 705
 RESULT 12
 V84254
 ID V84254 standard; cDNA; 2340 BP.
 AC V84254;
 DT 12-APR-1999 (first entry)
 DE Human uncoupling protein 3 (UCP3) cDNA.
 KW Uncoupling protein 3; UCP3; human; obesity; diabetes;
 KW hyperinsulinaemia; hypermetabolism; gene therapy; ds.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT CDS 344..1282
 FT /*tag= a
 FT /*note= "this region is specifically claimed in
 Claim 2"
 PN W09852958-A1.
 PD 26-NOV-1998.
 PF 19-MAY-1998; U10215.
 PR 09-DEC-1997; US-069141.
 PR 20-MAY-1997; US-047179.
 PR 08-AUG-1997; GB-016886.
 PA (MERI) MERCK & CO INC.
 PI Chen F, Liu Q;
 DR WPI: 99-059737/05.
 DR P-PSDB: W88279.
 PT New isolated human uncoupling protein 3 - used to identify compounds
 PT which can modulate energy expenditure and body weight regulation,
 PT e.g. in the treatment of obesity or diabetes.
 PS Claim 1; Page 57-58; 87pp; English.
 CC This cDNA clone encodes human uncoupling protein 3 (UCP3, see
 CC W88279), a novel protein that is involved in energy expenditure and
 CC body weight regulation and whose expression is mostly limited to
 CC skeletal muscle. The clone was isolated from a foetal brain cDNA
 CC library using primers (see V84259-64) based on isolated EST clones
 CC (see V84255-58) and paluescript vector sequences. The invention
 CC additionally provides related recombinant expression vectors,
 CC recombinant host cells and purified forms of the UCP3 protein.
 CC The UCP3 polypeptides and transformed recombinant cell lines can

CC be used for identifying modulators of UCP3 activity. Such
 CC modulators can be used for treating diseases such as obesity and
 CC diabetes, by manipulating the interrelated process of balancing
 CC food intake, energy expenditure and glucose metabolism within the
 CC patient. They can also be used to treat hyperactive conditions of
 CC energy expenditure which originate in the mitochondria of skeletal
 CC muscle. UCP3 nucleic acids are useful in gene therapy of obesity
 CC and obesity-related indications, including diabetes, and of
 CC mitochondrial-associated hypermetabolism.
 CC Sequence 2340 BP; 606 A; 638 C; 463 T;
 SQ

Query Match 64.3%; Score 14.8; DB 1; Length 2340;
 Best Local Similarity 61.9%; Pred. No. 73;
 Matches 13; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 cngtngartgaayttgcnm 22
 Db 875 CTGTGGAAAGGACTTTCGCC 895

RESULT 13
 N92579/c
 ID N92579 standard; DNA; 3094 BP.
 AC N92579;
 DT 15-MAR-1992 (first entry)
 DE Sequence of the 1.7kb cDNA molecule encoding antibodies 7DL,7D4
 DE and 20C6.
 CC KW Vaccine; coccidiosis; poultry; bivalent vaccine; ss.
 OS Eimeria.
 FH Key Location/Qualifiers
 FT cds 9..3002 /*tag= a
 FT EP-344808-A.
 PN 06-DEC-1989.
 PF 02-JUN-1989; 110056.
 PD 03-JUN-1988; US-202721.
 PR (HOFF) HOFFMANN-LA ROCHE AG.
 PA Altenburger W, Binger MH, Chizzonite RA, Kramer RA,
 PI Lomedico PT, McAndrew SJ;
 DR WPI; 89-358220/49.
 DR P-PSDB; P93706.
 PT DNA sequences encoding Eimeria surface antigens - used in
 PT pox:virus vectors as a vaccine to protect chicks against
 PT coccidiosis
 FT Claim 10; Fig 20A-D; 78pp; English.
 PS The inventors claim a new protein which comprises one or more
 CC immunoreactive and/or antigenic determinants of an Eimeria surface
 CC antigen of mol. wt. 28,37,120 or more than 200 kD which specifically
 CC binds to one or more monoclonal antibody (MaB) from ATCC HB 9707-9712
 CC (see P93703-6). Also new are DNA encoding the protein (see N92576-9),
 CC and a vaccine comprising one or more proteins. Vaccine utility can
 CC be enhanced by inserting additional genes into the carrier virus
 CC (see P91652).
 CC Sequence 3094 BP; 617 A; 834 C; 846 G; 796 T;
 SQ

Query Match 63.5%; Score 14.6; DB 1; Length 3094;
 Best Local Similarity 63.6%; Pred. No. 97;
 Matches 14; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 gcngtngartgaayttgcnm 22
 Db 262 GCAGGGGAGTGGAGTTCGCGA 241

RESULT 14
 T93597/c
 ID T93597 standard; cDNA; 2997 BP.
 AC T93597;
 DT 21-MAY-1998 (first entry)
 DE Eimeria tenella sporozoite 45 kDa surface antigen cDNA.
 DE Coccidiosis; vaccine; poultry; protozoan; parasite; antigen;
 KW

KW sporozoite; ss.
 OS Eimeria tenella.
 FH Key Location/Qualifiers
 FT cds 7..2997 /*tag= a
 FT US5661015-A.
 PN 26-AUG-1997.
 PF 03-JUN-1988; 202721.
 PR 20-DEC-1991; US-812349.
 PR 03-JUN-1988; US-202721.
 PR (HOFF) HOFFMANN LA ROCHE INC.
 PA Altenburger W, Binger M, Chizzonite RA, Kramer RA,
 PI Lomedico PT, McAndrew SJ;
 DR WPI; 97-434379/40.
 DR P-PSDB; W33624.
 DT New DNA from Eimeria tenella and related immunogenic polypeptides -
 DT useful in vaccines to protect poultry against coccidiosis
 PS Claim 2; Fig 33A-B; 72pp; English.
 CC This cDNA sequence comprises the coding region for a 45 kDa protein
 CC (see W33624) that is recognised by monoclonal antibody 7B2
 CC (ATCC HB 9712). This antibody also specifically reacts with an
 CC Eimeria tenella 200 kDa surface antigen that is present in the
 CC sporozoite developmental stage. The clone (see also T93596) was
 CC obtained from a cDNA library by immunological screening with
 CC monoclonal antibodies raised against Eimeria antigens. The
 CC invention provides DNA sequences (see T93593-98) coding for Eimeria
 CC surface antigens (see W1582-84 and W33621-26), recombinant vectors
 CC containing such DNA sequences, transformed microorganisms
 CC using the transformed microorganisms. Methods are also provided
 CC for protecting poultry against coccidiosis using the Eimeria
 CC surface antigens. The surface antigens are administered either as
 CC purified proteins or in the form of DNA encoding the proteins in
 CC a viral vector such as a vaccinia virus. The vaccines may produce
 CC antibodies that are cross-reactive with other Eimeria species.
 CC Sequence 2997 BP; 583 A; 815 C; 830 G; 769 T;
 SQ

Query Match 63.5%; Score 14.6; DB 1; Length 2997;
 Best Local Similarity 63.6%; Pred. No. 97;
 Matches 14; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 gcngtngartgaayttgcnm 22
 Db 254 GCAGGGGAGTGGAGTTCGCGA 233

RESULT 15
 T93596/c
 ID T93596 standard; cDNA; 3094 BP.
 AC T93596;
 DT 21-MAY-1998 (first entry)
 DE Eimeria tenella sporozoite 45 kDa surface antigen cDNA.
 DE Coccidiosis; vaccine; poultry; protozoan; parasite; antigen;
 KW Sporozoite; ss.
 OS Eimeria tenella.
 FH Key Location/Qualifiers
 FT cds 9..3005 /*tag= a
 FT /transl_except= (pos:600..602, aa:Tyr)
 FT /transl_except= (pos:603..605, aa:Ser)
 FT /transl_except= (pos:606..608, aa:Gly)
 FT /transl_except= (pos:612..614, aa:Ala)
 FT /transl_except= (pos:615..617, aa:Leu)
 FT /transl_except= (pos:618..620, aa:Ala)
 FT misc_difference 2001
 FT /*tag= b
 FT /note= "base 2001 is given as '8' in Fig20
 FT of the specification"
 FT US5661015-A.
 PN 26-AUG-1997.
 PD 03-JUN-1988; 202721.
 PR 20-DEC-1991; US-812349.

Fri Oct 1 16:47:13 1999

PR 03-JUN-1988; US-202721.
 PA (HOFF) HOFFMANN LA ROCHE INC.
 PI Altenburger W, Binger M, Chizzonite RA, Kramer RA,
 PI Lomedico PT, McAndrew SJ;
 DR WPI: 97-434379/40.
 DR P-PSDB; W33621.
 CC New DNA from Eimeria tenella and related immunogenic polypeptides -
 PT useful in vaccines to protect poultry against coccidiosis
 PS Claim 1; Fig 20A-D; 72pp; English.
 CC This cDNA clone includes a coding region for a 45 kDa protein (see
 CC W33621) that is recognised by monoclonal antibody 7B2 (ATCC HB 9712).
 CC This antibody also specifically reacts with an Eimeria tenella 200
 CC kDa surface antigen that is present in the sporozoite developmental
 CC stage. The clone was obtained from a cDNA library by immunological
 CC screening with monoclonal antibodies raised against Eimeria
 CC antigens. The first and last 7 nucleotides of the sequence are
 CC derived from linker sequences used in the cloning procedure. The
 CC invention provides DNA sequences (see T93593-98) coding for Eimeria
 CC surface antigens (see W31582-84 and W33621-26), recombinant vectors
 CC containing such DNA sequences, transformed microorganisms
 CC containing such vectors, and methods for producing the antigens
 CC using the transformed microorganisms. Methods are also provided
 CC for protecting poultry against coccidiosis using the Eimeria
 CC surface antigens. The surface antigens are administered either as
 CC purified proteins or in the form of DNA encoding the proteins in
 CC a viral vector such as a vaccinia virus. The vaccines may produce
 CC antibodies that are cross-reactive with other Eimeria species.
 SQ Sequence 3094 BP; 619 A; 834 C; 844 G; 796 T;

Query Match 63.5%; Score 14.6; DB 1; Length 3094;
 Best Local Similarity 63.6%; Pred. No. 97;
 Matches 14; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 gcngtngartggaaytttgcnm 22
 ||| ||||| ||||| :
 Db 262 GCAGGGGAGTGGAGTTCGCGA 241

Search completed: October 1, 1999, 15:36:18
 Job time: 6116 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 1, 1999, 15:03:35 ; Search time 1096.08 Seconds
(without alignments)
41.391 Million cell updates/sec

Title: US-09-026-400-5
Perfect score: 23
Sequence: 1 gcngtngartggaaytygcmng 23

Scoring table: IDENTITY_NUC

Searched: 2546578 seqs, 986266752 residues

Database :

EST.*

- 1: em_est1.*
- 2: em_est2.*
- 3: em_est3.*
- 4: em_est4.*
- 5: em_est5.*
- 6: em_est6.*
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- 8: em_est8.*
- 9: em_est9.*
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- 18: em_est18.*
- 19: em_est19.*
- 20: gb_est1.*
- 21: gb_est2.*
- 22: gb_est3.*
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- 28: gb_est9.*
- 29: gb_est10.*
- 30: gb_est11.*
- 31: gb_est12.*
- 32: gb_est13.*
- 33: gb_est14.*
- 34: gb_est15.*
- 35: gb_est16.*
- 36: gb_est17.*
- 37: gb_est18.*
- 38: gb_est19.*
- 39: gb_est20.*
- 40: gb_est21.*
- 41: gb_est22.*
- 42: gb_est23.*
- 43: gb_est24.*
- 44: gb_est25.*
- 45: gb_est26.*
- 46: gb_est27.*
- 47: gb_est28.*
- 48: gb_est29.*
- 49: gb_est30.*
- 50: gb_est31.*
- 51: gb_est32.*
- 52: em_est20.*
- 53: em_est21.*

- 54: em_est22.*
- 55: em_est23.*
- 56: em_est24.*
- 57: em_est25.*
- 58: em_est26.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	16.8	73.0	693	36	AA660414	AA660414 00290 MTR
C 2	15.8	68.7	539	22	H11322	H11322 yml3a03.s1
C 3	15.8	68.7	433	22	H13911	H13911 yj08g05.r1
C 4	15.8	68.7	281	23	H56483	H56483 yf87e12.s1
C 5	15.8	68.7	463	24	H98744	H98744 yx12c12.s1
C 6	15.8	68.7	421	25	W08531	W08531 mb47b04.r1
C 7	15.8	68.7	528	26	W41942	W41942 mc64e07.r1
C 8	15.8	68.7	447	26	W60228	W60228 zd28g09.s1
C 9	15.8	68.7	470	26	W76544	W76544 zd60q09.s1
C 10	15.8	68.7	324	27	AA003148	AA003148 mg51g01.r
C 11	15.8	68.7	432	27	AA010775	AA010775 ze22f04.r
C 12	15.8	68.7	497	27	AA036822	AA036822 zk29b05.r
C 13	15.8	68.7	360	27	AA038824	AA038824 mi95g07.r
C 14	15.8	68.7	603	27	AA057660	AA057660 zl93d09.s
C 15	15.8	68.7	430	27	W82322	W82322 mf04g11.r1
C 16	15.8	68.7	420	27	W82575	W82575 mf04a11.r1
C 17	15.8	68.7	390	28	AA059678	AA059678 mj75d09.r
C 18	15.8	68.7	495	28	AA060109	AA060109 mj71g12.r
C 19	15.8	68.7	542	28	AA061890	AA061890 mj92h08.r
C 20	15.8	68.7	490	28	AA075167	AA075167 zm86g04.s
C 21	15.8	68.7	553	28	AA082814	AA082814 zn25b04.r
C 22	15.8	68.7	417	28	AA103480	AA103480 mo24h04.r
C 23	15.8	68.7	454	29	AA132788	AA132788 zo22d08.s
C 24	15.8	68.7	415	29	AA145601	AA145601 mr63f03.r
C 25	15.8	68.7	586	29	AA147813	AA147813 zo48b09.s
C 26	15.8	68.7	437	29	AA151511	AA151511 zl36h07.r
C 27	15.8	68.7	336	29	AA183476	AA183476 mo97f03.r
C 28	15.8	68.7	555	29	AA187994	AA187994 zp87h06.s
C 29	15.8	68.7	442	30	AA206634	AA206634 zq80c11.s
C 30	15.8	68.7	563	30	AA222589	AA222589 mv70b12.r
C 31	15.8	68.7	476	30	AA243010	AA243010 zr25h03.s
C 32	15.8	68.7	485	30	AA250948	AA250948 zs06h11.r
C 33	15.8	68.7	334	30	AA269452	AA269452 va90a06.r
C 34	15.8	68.7	406	32	AA336931	AA336931 ES41591
C 35	15.8	68.7	521	33	AA447651	AA447651 zw97g04.s
C 36	15.8	68.7	544	34	AA472282	AA472282 vhl01b03.r
C 37	15.8	68.7	372	34	AA474481	AA474481 vd55e09.r
C 38	15.8	68.7	367	34	AA475447	AA475447 vhl5a11.r
C 39	15.8	68.7	545	34	AA516883	AA516883 vh88h03.r
C 40	15.8	68.7	552	34	AA521284	AA521284 aa275h07.s
C 41	15.8	68.7	423	35	AA555952	AA555952 vi64g01.r
C 42	15.8	68.7	584	35	AA594843	AA594843 no21b08.s
C 43	15.8	68.7	694	36	AA640937	AA640937 nr72e09.s
C 44	15.8	68.7	435	36	AA662313	AA662313 nu97d03.s
C 45	15.8	68.7	503	47	AI540076	AI540076 td09a05.x

ALIGNMENTS

RESULT 1
AA660414/c
LOCUS AA660414 693 bp mRNA EST 10-NOV-1997
DEFINITION 00290 MTRHE Medicago truncatula cDNA 5', mRNA sequence.
ACCESSION AA660414
NID 92604458
VERSION AA660414.1 GI:2604458
KEYWORDS EST.

SOURCE
ORGANISM
barrel medic.
Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae;
Medicago.
1 (bases 1 to 693)
Covitz, P.A., Smith, L.S. and Long, S.R.
Expressed sequence tags from a root hair-enriched Medicago
truncatula cDNA library
Unpublished (1997)
JOURNAL
On Sep 12, 1996 this sequence version replaced gi:1290520.
COMMENT
Contact: Long SR
Department of Biological Sciences and Howard Hughes Medical
Institute
Stanford University
Gilbert Biology, Stanford, CA 94305-5020, USA
Tel: 650 723 3232
Fax: 650 725 8309
Email: fa.srl@forsthe.stanford.edu
Seq primer: T3.
FEATURES
source
1..693
/organism="Medicago truncatula"
/cultivar="Jemalong"
/db_xref="taxon:3880"
/clone_lib="MtrHE"
/tissue_type="Root hairs & tips"
/dev_stage="2-3 day old seedlings"
/note="Organ: Root; Vector: pBK-CMV; Site_1: EcoRI;
Site_2: XhoI; cDNA was synthesized from a pooled mRNA prep
from elongating root hairs (30% w/w) and 2-3cm root tips
(70% w/w). XhoI-oligo-dT linker-primer and EcoRI
adaptors were used. cDNAs were cloned unidirectionally
into lambda ZAP Express (Stratagene), amplified, and
mass-excised into pBK-CMV vector plasmids. More
information is available at http://bio-SRL8.stanford.edu."
BASE COUNT 187 a 149 c 133 g 178 t 46 others
ORIGIN
Query Match 73.0%; Score 16.8; DB 36; Length 693;
Best Local Similarity 65.2%; Pred. No. 38;
Matches 15; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
Qy 1 gcngtngartggaayttgcmng 23
||| |||:||||:||||:|
Db 206 GCAGTGAGTGAATTTGCACG 184
RESULT 2
H11322/c 539 bp mRNA EST 26-JUN-1995
LOCUS ym13a03.s1 Soares infant brain 1N1B Homo sapiens cDNA clone
DEFINITION IMAGE:47520 3', mRNA sequence.
ACCESSION H11322
NID G876142
VERSION H11322.1 GI:876142
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 539)
AUTHORS Hillier, L., Clark, N., Dubucq, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and
Wilson, R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT On May 10, 1995 this sequence version replaced gi:805432.
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 1450
High quality sequence stops: 410
Source: IMAGE Consortium, LNL
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Insert Length: 1450 Std Error: 0.00
Seq primer: Promega -2lml3
High quality sequence stop: 410.
FEATURES
Location/Qualifiers
1..539
/organism="Homo sapiens"
/db_xref="GDB:420061"
/db_xref="taxon:9606"
/clone="IMAGE:47520"
/clone_lib="Soares infant brain 1N1B"
/sex="female"
/dev_stage="73 days post natal"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: whole brain; Vector: Lfamid BA; Site_1: Not
I; Site_2: Hind III; 1st strand cDNA was primed with a Not
I - oligo(dT) primer [5',
ACTGGAAAGATTCGGCGCGAGGAATTTTITTTTTT 3'];
double-stranded cDNA was ligated to Hind III adaptors
(Pharmacia), digested with Not I and directionally cloned
into the Not I and Hind III sites of the Lfamid BA vector.
Library went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bernaldo."
BASE COUNT 135 a 132 c 131 g 135 t 6 others
ORIGIN
Query Match 68.7%; Score 15.8; DB 22; Length 539;
Best Local Similarity 63.6%; Pred. No. 1.3e+02;
Matches 14; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
Qy 2 cngtngartggaayttgcmng 23
||| |||:||||:||||:|
Db 453 CAGTTGAGGGGAACTTTGCCAG 432
RESULT 3
H13911 433 bp mRNA EST 27-JUN-1995
LOCUS y708g05.r1 Soares placenta ND2HP Homo sapiens cDNA clone
DEFINITION IMAGE:148184 5', mRNA sequence.
ACCESSION H13911
NID G878731
VERSION H13911.1 GI:878731
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 433)
AUTHORS Hillier, L., Clark, N., Dubucq, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and
Wilson, R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800

Fax: 314 286 1810
 Email: est@watson.wustl.edu
 Insert Size: 591
 High quality sequence stops: 331
 Source: IMAGE Consortium, LLNL
 This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Insert Length: 591 Std Error: 0.00
 Seq primer: M13RP1
 High quality sequence stop: 331.

FEATURES

Location/Qualifiers
 1..433
 /organism="Homo sapiens"
 /db_xref="GDB:559920"
 /db_xref="taxon:9606"
 /clone="IMAGE:148184"
 /clone_lib="Soares placenta Nb2Hp"
 /sex="Female"
 /dev_stage="placenta obtained at birth (full term)"
 /lab_host="DH10B (ampicillin resistant)"
 /note="Organ: placenta; Vector: pT73D (Pharmacia) with a
 modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
 strand cDNA was primed with a Not I - oligo(dT) primer [5'
 AACTGGAAGATTCGCGCGCAGCAATTTTTTTTTTTTTTTT 3'],
 double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Not I and cloned into the Not I
 and Eco RI sites of the modified pT73 vector. Library
 went through one round of normalization. Library
 constructed by Bento Soares and M.Fatima Bonaudo."

BASE COUNT 103 a 105 c 120 g 103 t 2 others
 ORIGIN

Query Match 68.7%; Score 15.8; DB 22; Length 433;

Best Local Similarity 63.6%; Pred. No. 1.2e+02; DB 22; Length 433;
 Matches 14; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 cngtngartggaaytygcnmg 23
 |||||:|||||:|:|:
 Db 108 CAGTTCGAGGGAAGTTCGAG 129

RESULT 4

H56483 281 bp mRNA EST 02-OCT-1995
 LOCUS
 DEFINITION Yt87el2.s1 Soares pineal_gland_N3HPG Homo sapiens cDNA clone
 IMAGE:231310 3' similar to gb:X71973 PHOSPHOLIPID HYDROPEROXIDE
 GLUTATHIONE PEROXIDASE (HUMAN);, mRNA sequence.

ACCESSION H56483
 NID 91005127
 VERSION H56483.1 GI:1005127
 KEYWORDS EST.
 SOURCE human.

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

AUTHORS Hillier,L., Lennon,G., Becker,M., Bonaudo,M.F., Chiappelli,B.,
 Chisoe,S., Dietrich,N., Dubuque,T., Favello,A., Gish,W.,
 Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,N.,
 Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L.,
 Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J.,
 Trevaskis,E., Underwood,K., Wohlmann,P., Waterston,R., Wilson,R.
 and Marra,M.

TITLE Generation and analysis of 280,000 human expressed sequence tags
 JOURNAL Genome Res. 6 (9), 807-828 (1996)
 MEDLINE 97044478

COMMENT On May 9, 1995 this sequence version replaced gi:803053.

Contact: Wilson RK

Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800

Fax: 314 286 1810
 Email: est@watson.wustl.edu

Insert Size: 1524

High quality sequence starts: 1

High quality sequence stops: 1

Source: IMAGE Consortium, LLNL
 This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.

Trace considered overall poor quality

Insert Length: 1524 Std Error: 0.00

Seq primer: Promega -2lm13

High quality sequence stop: 1.

FEATURES

Location/Qualifiers
 1..281
 /organism="Homo sapiens"
 /db_xref="GDB:3861301"
 /db_xref="taxon:9606"
 /clone="IMAGE:231310"
 /clone_lib="Soares pineal_gland_N3HPG"
 /lab_host="DH10B (ampicillin resistant)"
 /note="Organ: pineal gland; Vector: pT73D (Pharmacia)
 with a modified polylinker; Site_1: Not I; Site_2: Eco RI;
 1st strand cDNA was primed with a Not I - oligo(dT) primer
 [5' TGTTACCAATCTGAGTGGAGCGCCGCTTTTTTTTTTTT
 3'], double-stranded cDNA was size selected, ligated to
 Eco RI adaptors (Pharmacia), digested with Not I and
 cloned into the Not I and Eco RI sites of a modified pT73
 vector (Pharmacia). Library constructed by Bento Soares
 and M.Fatima Bonaudo."

BASE COUNT 45 a 81 c 92 g 53 t 10 others
 ORIGIN

Query Match 68.7%; Score 15.8; DB 23; Length 281;

Best Local Similarity 63.6%; Pred. No. 1.2e+02; DB 23; Length 281;

Matches 14; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 cngtngartggaaytygcnm 22
 |||||:|||||:|:|:
 Db 271 GCATAGAGTGGAGTTCGCCA 250

RESULT 5

H98744/c 463 bp mRNA EST 15-DEC-1995
 LOCUS
 DEFINITION Yx12c12.s1 Soares melanocyte 2NBHM Homo sapiens cDNA clone
 IMAGE:261526 3', mRNA sequence.

ACCESSION H98744
 NID 91123412
 VERSION H98744.1 GI:1123412
 KEYWORDS EST.
 SOURCE human.

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
 Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
 Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
 Trevaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and
 Wilson,R.

TITLE The WashU-Merck EST Project

JOURNAL

COMMENT Unpublished (1995)
 On Nov 22, 1995 this sequence version replaced gi:1071096.

Contact: Wilson RK

Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

High quality sequence stops: 377

Fri Oct 1 16:47:13 1999

Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 1012 Std Error: 0.00

Seq primer: ml3 -40 forward

High quality sequence stop: 377.

FEATURES

Location/Qualifiers
1. .463
/organism="Homo sapiens"
/db_xref="GDB:3871168"
/db_xref="taxon:9606"
/clone="IMAGE:261526"
/clone_lib="Soares melanocyte 2NbHM"
/sex="Male"
/tissue_type="melanocyte"
/lab_host="DH10B (ampicillin resistant)"
/note="Vector: pT73D (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5',
TGTTCACATCTGAAGTGGAGCGCCGCGCATTTTCTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library constructed by Bento Soares and
M.Fatima Bonaldo. RNA from normal foreskin melanocytes
(FS374) was kindly provided by Dr. Anthony P. Albino."
123 a 122 c 110 g 107 t 1 others

BASE COUNT

ORIGIN
Query Match 68.7%; Score 15.8; DB 24; Length 463;
Best Local Similarity 63.6%; Pred. No. 1.2e+02;
Matches 14; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 cngtngartggaaytygcnmg 23

Db 433 CAGTTGAGGGAACTTTGCCAG 412

RESULT

W08531 6
LOCUS 421 bp mRNA EST 05-SEP-1996
DEFINITION mb47b04.r1 Soares mouse p3NMF19.5 Mus musculus cDNA clone
IMAGE:332527 5', mRNA sequence.
ACCESSION W08531
NID G1282533
VERSION G1282533
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS 1 (bases 1 to 421)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
TITLE The WashU-HHMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT On Nov 29, 1993 this sequence version replaced gi:430122.

Contact: Marra M/Mouse EST Project

WashU-HHMI Mouse EST Project

Washington University School of MedicineP

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@wustl.edu

This clone is available royalty-free through LLNL ; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:213927

Seq primer: ETPrimer

FEATURES

Location/Qualifiers
1. .421

/organism="Mus musculus"

/db_xref="taxon:10090"

/map="1"

/clone="IMAGE:332527"

/clone_lib="Soares mouse p3NMF19.5"

/dev_stage="19.5 dpc total fetus"

/lab_host="DH10B (ampicillin resistant)"

/note="Vector: pT73D (Pharmacia) with a modified

polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA

was primed with a Not I - oligo(dT) primer [5',

TGTTCACATCTGAAGTGGAGCGCCGCGCATTTTCTTTT 3'],

double-stranded cDNA was size selected, ligated to Eco RI

adapters (Pharmacia), digested with Not I and cloned into

the Not I and Eco RI sites of a modified pT73 vector

(Pharmacia). Library went through one round of

normalization to a Cot = 5. Library constructed by Bento

Soares and M.Fatima Bonaldo. RNA was kindly provided by

Dr. Minoru Ko (Wayne State University)."

93 a 115 c 123 g 90 t

BASE COUNT

ORIGIN
Query Match 68.7%; Score 15.8; DB 25; Length 421;
Best Local Similarity 63.6%; Pred. No. 1.2e+02;
Matches 14; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 cngtngartggaaytygcnmg 23

Db 104 CAGTTGAGGGAACTTTGCCAG 125

RESULT

W41942 7
LOCUS 528 bp mRNA EST 20-MAY-1996
DEFINITION mc64e07.r1 Soares mouse embryo NME13.5 14.5 Mus musculus cDNA
clone IMAGE:353316 5', mRNA sequence.
ACCESSION W41942
NID G1325656
VERSION W41942.1 GI:1325656
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS 1 (bases 1 to 528)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
TITLE The WashU-HHMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT On Apr 14, 1993 this sequence version replaced gi:693673.

Contact: Marra M/Mouse EST Project

WashU-HHMI Mouse EST Project

Washington University School

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@wustl.edu

This clone is available royalty-free through LLNL ; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:225116

Seq primer: ETPrimer

High quality sequence stop: 301.

Location/Qualifiers

1. .528

/organism="Mus musculus"

/strain="C57BL/6J"

Fri Oct 1 16:47:13 1999

```
/db_xref="taxon:10090"
/clone="IMAGE:353316"
/lab_lib="Soares mouse embryo NBME13.5 14.5"
/sex="unknown"
/tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand
CDNA was primed with a Not I - oligo(dT) primer [5',
TGTTACCAATCTGAAGTGGGAGCGCGCGAATTTTTTTTTTTTTTTT
T 3'], on equal amounts of mRNA from 2 13.5dpc and 2
14.5dpc embryos [total RNA provided by Minoru Ko, Wayne
State Univ., from 2 ]; double-stranded CDNA was ligated to
Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
pT73 vector. Library went through one round of
normalization, and was constructed by Bento Soares and
M.Fatima Bonaldo."
BASE COUNT      129 a  134 c  148 g  117 t
ORIGIN

Query Match      68.7%; Score 15.8; DB 26; Length 528;
Best Local Similarity 63.6%; Pred. No. 1.3e+02;
Matches 14; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY  2  cngtngartggaaytytgcnmg 23
      |||||:||||:||||:|
Db  141 CAGTTGAGGGGAACCTTGCCAG 162

RESULT  8
W60228/c
LOCUS      W60228      447 bp  mRNA      EST      15-OCT-1996
DEFINITION z028509.s1 Soares_fetal_heart_NBHH19W Homo sapiens CDNA clone
IMAGE:342016 3', mRNA sequence.
ACCESSION  W60228
NID        G1366989
VERSION    W60228.1 GI:1366989
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1 (bases 1 to 447)
AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Watson,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
            The WashU-Merck EST Project
            Unpublished (1995)
            On Oct 18, 1995 this sequence version replaced gi:1023563.

TITLE     The WashU-Merck EST Project
JOURNAL   Unpublished (1995)
COMMENT   On Oct 18, 1995 this sequence version replaced gi:1023563.

Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 857 Std Error: 0.00
Seq primer: mob.REGA+ET
High quality sequence stop: 405.

FEATURES             source
     source
     1..447
     /organism="Homo sapiens"
     /db_xref="GDB:1267391"
     /db_xref="taxon:9606"
     /clone="IMAGE:342016"
     /clone_lib="Soares_fetal_heart_NBHH19W"

/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: heart; Vector: pT73D (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand CDNA was primed with a Not I - oligo(dT) primer [5',
TGTTACCAATCTGAAGTGGGAGCGCGCGAATTTTTTTTTTTTTTTT 3']
double-stranded CDNA was size selected, ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by
M.Fatima Bonaldo. This library was constructed from the
same fetus as the fetal lung library, Soares fetal lung
NBHH19W."
BASE COUNT      117 a  116 c  104 g  108 t  2 others
ORIGIN

Query Match      68.7%; Score 15.8; DB 26; Length 447;
Best Local Similarity 68.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY  2  cngtngartggaaytytgcnmg 23
      |||||:||||:||||:|
Db  443 CAGTNGAGGGGAACCTTGCCAG 422

RESULT  9
W76544/c
LOCUS      W76544      470 bp  mRNA      EST      16-OCT-1996
DEFINITION z060d09.s1 Soares_fetal_heart_NBHH19W Homo sapiens CDNA clone
IMAGE:345041 3', mRNA sequence.
ACCESSION  W76544
NID        G1386779
VERSION    W76544.1 GI:1386779
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
            Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1 (bases 1 to 470)
AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Watson,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
            The WashU-Merck EST Project
            Unpublished (1995)
            On Apr 14, 1993 this sequence version replaced gi:716583.

TITLE     The WashU-Merck EST Project
JOURNAL   Unpublished (1995)
COMMENT   On Apr 14, 1993 this sequence version replaced gi:716583.

Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1070 Std Error: 0.00
Seq primer: mob.REGA+ET
High quality sequence stop: 414.

FEATURES             source
     source
     1..470
     /organism="Homo sapiens"
     /db_xref="GDB:1270416"
     /db_xref="taxon:9606"
     /map="5 q13: 754A01; 12: 12q12-12q13.13"
     /clone="IMAGE:345041"
     /clone_lib="Soares_fetal_heart_NBHH19W"
     /sex="unknown"
     /dev_stage="19 weeks"
     /lab_host="DH10B (ampicillin resistant)"
```

/notes="Organ: heart; Vector: pT73D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCAATCTGAAGTGGAGCGGCAGCTTTTTTTTTTTTTTTT 3'], TGTGTTACCAATCTGAAGTGGAGCGGCAGCTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by M.Patima Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung vbr1.19g."

BASE COUNT	122 a	126 c	113 g	109 t
ORIGIN	NORTHAM.			

```
Query Match      68.7%; Score 15.8; DB 26; Length 470;
Best Local Similarity 63.6%; Pred. No. 1.2e+02;
Matches 14: Conservative 4; Mismatches 4; Indels 0; Gaps 0;
```

Qy 2 cngtngartggaayttygcnmg 23
 — || ||: ||||: ||: ||: ||
 Db 435 CAGTTGAGGGGAACCTTGGCCAG 414

RESULT	10
AA003148	
LOCUS	
DEFINITION	mg51g01.r1 Soares mouse embryo NBMel3.5 14.5 EST
	clone TWAGE:437344 5'. mRNA sequence.
	AA003148 324 bp mRNA
	19-JUL-1996 Mus musculus cDNA

AA003148
g1446605
AA003148.1 GI:1446605
EST.

SOURCE	ORGANISM
house mouse.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Mus musculus
	Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
1 (bases 1 to 324)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Thelising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.

TITLE The WashU-HHMI Mouse EST Project
JOURNAL Unpublished (1996)

JOURNAL COMMENT

Contact: Marra M/Mouse EST Project
WashU-HIMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810

Fax: 314 200 1010
 Email: mouseeet@watson.wustl.edu
 This clone is available royalty-free through LLNL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:261896

MG1:261896
500 primer: FTDprimer

seq primer: ETPPrimer
High quality sequence stop: 287.

FEATURES	source
Location/Qualifiers	1. .324
	/organism="Mus musculus"
	/strain="C57BL/6J"
	/db_xref="taxon:10090"
	/clone="IMAGE:427344"
	/clone_lib="Spares mouse embryo NDBE13.5 14.5"

```

/tissue_type="embryo"
/dev stage="13.5-14.5dpc total fetus"

```

```

/rev_stage="DH10B"
/lab_host="DH10B"
/note="Vector: pT7T3b-Pac (Pharmacia) with a modified
polylinker: Site 1: Not I; Site 2: Eco RI; 1st strand
CDNA

```

was primed with a Not I - oligo(dT) primer [5', TGTTCACCAATCTGAAGTGGAGCGCCGGAATTTTTTTTTTTTTTTTTTTTTTTTTTTT 3'], on equal amounts of mRNA from 2 13.5dpc and 2 14.5dpc embryos [total RNA provided by Minoru KO, Wayne State Univ., from 2]; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo.

BASE COUNT	79 a	90 c	94 g	61 t
ORIGIN				

Query Match 68.7%; Score 15.8; DB 27; Length 324;
Best Local Similarity 63.6%; Pred. NO. 1.2e+02;

QY 2 cngtngartggaayttygcnmg 23
| | | | | : | | | | : |
Dh 109 CACTTCAGGGGAACCTTTGCCAG 130

RESULT	11
AA010775	
LOCUS	
DEFINITION	AA010775 432 bp mRNA EST 29-NOV-1996 ze22f04.r1 Soares fetal heart NBH19W Homo sapiens cDNA clone IMAGE:359743 5', mRNA sequence.

ACCESSION AA010775
NID 91471802
VERSION AA010775.1 GI:1471802
KEYWORDS EST.
SOURCE human.

SOURCE	ORGANISM	HOMO sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;	
	Eutheria; Primates; Catarrhini; Homiidae; Homo.	

REFERENCE
AUTHORS
1 (pages 1 to 432)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
Wilson, R.

TITLE The WashU-Merck EST Project

JOURNAL
Unpublished (1995)
On Apr 14, 1993 this sequence version replaced qi:785787.
COMMENT

Contact: Wilson RK
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Tel: 314 286 1800

Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (infoimage.llnl.gov) for further information.
Insert Length: 697 Std Error: 0.00
Fax: 314 286 1810

Seq primer: mob.REGA+ET
High quality sequence stop: 346.

FEATURES	SOURCE
----------	--------

```
l...%32  
/organism="Homo sapiens"  
/db_xref="GB|1276287"  
/db_xref="taxon:9606"  
/map="4 q35-qter"  
/clone.lib="IMAGE:359743"  
/clone.lib="Soares_fetal_heart_NbHH19W"  
/sex="unknown"  
/dev_stage="19 weeks"  
/lab_host="DfIB0 (ampicillin resistant)"  
/notes="Organ: heart; Vector: pTR3B (Phar  
modified polylinker; Site_1: Site  
strand cDNA was primed with a Not I - ol  
TGTTACCAATCTGAAGTCGAGCGGCAGCATTTTTT  
double-stranded cDNA was size selected,
```

Query Match 68.7%; Score 15.8; DB 27; Length 360;
Best Local Similarity 63.6%; Pred. No. 1.2e+02;

Matches	14	Conservative	4	Mismatches	4	Indels	0	Gaps	0
---------	----	--------------	---	------------	---	--------	---	------	---

Qy 2 cngtngartggaayttygcnmg 23
| | | | | : | | | | : |
Db 299 CAGTTGAGGGGAACCTTGCCAG 320

RESULT	14
AA057660/c	
LOCUS	AA057660 603 bp mRNA EST 19-MAY-1997
DEFINITION	Zl9sd09.s1 Stratagene corneal stroma (#937222) Homo sapiens cDNA clone IMAGE:512177 3' similar to TR:G1255188 G1255188 DYNAMITIN.; mRNA sequence.

NID 91330300
VERSION AA057660.1 GI:1550300
KEYWORDS EST.
SOURCE human.

SOURCE	ORGANISM	Human:
	<i>Homo sapiens</i>	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;	
	Eutheria; Primates; Catarrhini; Hominoidea; Homo.	

REFERENCE
AUTHORS

1. (bases 1 to 603)
Hillier, L., Lennon, G., Becker, M., Bonardo, M.F., Chiapelli, B.,
Chissos, S., Dietrich, N., DuBucque, T., Favellio, A., Gish, W.,
Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N.,
Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L.,
Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J.,
Trevaskis, E., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R.,
and Maria, M.

TITLE	Generation and analysis of 280,000 human expressed sequence tags
JOURNAL	Genome Res. 6 (9), 807-828 (1996)
MEDLINE	97044478
COMMENT	On Sep 12, 1996 this sequence version replaced gi:1297673.

Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1942 Std Error: 0.00
Seq primer: -40M13 fwd. from Amersham
High quality sequence stop: 470.

```

FEATURES
source
    Location/Qualifiers
        1..603
            /organism="Homo sapiens"
            /db_xref="GDB:3844673"
            /db_xref="taxon:9606"
            /map="12"
            /clone="IMAGE:512177"
            /clone_lib="Stratagene corneal stroma (#937222)"
            /dev_stage="76 years"
            /lab_host="SOLR cells (kanamycin resistant)"
            /note="Organ: cornea; Vector: pBluescript SK-; S
            EcORI: Site.2: XhoI: Cloned unidirectionally.
            Oligo dT: Corneal fibroblasts grown from explant
            years. Average insert size: 1.5 kb; Uni-ZAP XR V
            adaptor sequence: 5' GAATTCGCACGAG 3' -3' adapt
            sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'
            150 a 150 c 148 t 2 others
BASE COUNT

```

Query Match 68.7%; Score 15.8; DB 27; Length 603;
Best Local Similarity 63.6%; Pred. NO. 1.3e+02;
Matches 14; Conservative 4; Mismatches 4; Indels 0

Qy 2 cngtngartggaayttygcnmg 23
| | | | | : |
Db 439 CAGTTGAGGGGAACCTTTGCCAG 418

RESULT 15

W82322	LOCUS	DEFINITION
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95	95	95
96	96	96
97	97	97
98	98	98
99	99	99
100	100	100

ACCESSION
NID
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE AUTHORS

TITLE	JOURNAL	COMMENT
1. The Role of the Teacher in the 21st Century	Journal of Educational Research	1. The author argues that the teacher's role is becoming increasingly complex and multifaceted in the 21st century. This is due to the rapid pace of technological change and the increasing diversity of the student population. The teacher must now be a facilitator of learning, rather than a sole source of knowledge. This requires a shift in the teacher's mindset and a focus on developing students' critical thinking and problem-solving skills. The author also discusses the importance of collaboration and communication in the classroom, and the need for ongoing professional development for teachers.
2. The Impact of Social Media on Education	Journal of Educational Research	2. The author discusses the impact of social media on education, both in terms of its potential benefits and its potential drawbacks. On the one hand, social media can provide a platform for collaboration and communication between students and teachers, and it can be used to share resources and information. On the other hand, social media can also be a source of distraction and distraction, and it can be used to spread misinformation and hate speech. The author argues that educators need to be aware of these risks and to take steps to mitigate them. This includes setting clear guidelines for social media use in the classroom and providing students with the skills they need to use social media responsibly.
3. The Importance of Cultural Competence in Education	Journal of Educational Research	3. The author emphasizes the importance of cultural competence in education, particularly in a diverse society like the United States. Cultural competence refers to the ability to understand, appreciate, and interact with people from different cultures. The author argues that educators need to be culturally competent in order to provide a high-quality education for all students. This requires a focus on developing students' cultural awareness and understanding, and it also requires educators to reflect on their own cultural biases and assumptions. The author also discusses the importance of creating a culturally inclusive classroom environment, and the need for ongoing professional development for educators.
4. The Role of Technology in the Classroom	Journal of Educational Research	4. The author discusses the role of technology in the classroom, and the potential benefits and challenges of using technology in education. Technology can be used to enhance learning and provide students with personalized instruction, but it can also be a source of distraction and distraction. The author argues that educators need to be thoughtful about how they use technology in the classroom, and to focus on using technology to support learning rather than just for the sake of using it. This includes providing students with the skills they need to use technology effectively, and it also requires ongoing professional development for educators.
5. The Importance of Assessment in Education	Journal of Educational Research	5. The author discusses the importance of assessment in education, and the different types of assessment that can be used to measure student learning. Assessment is a key part of the educational process, and it can be used to provide feedback to students and to inform instruction. The author argues that educators need to use a variety of assessment methods, including formative and summative assessment, to get a complete picture of student learning. This includes using a variety of assessment tools, such as quizzes, tests, and projects, and it also requires ongoing professional development for educators.

Contact: Marra M/Mouse EST Project
WasU-HHMI Mouse EST Project
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IMAGE Consortium (info@image.llnl.gov) for further information.

Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 393.

FEATURES

1. 430
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:404132"
/clone_lib="Soares mouse p3NNF19.5"
/dev_stage="19.5 dpc total fetus"
/lab_host="DH10B (ampicillin resistant)"
/note="Vector: pT73D (Pharmacia) with a modified
polylinker. Site1: Not I; Site2: Eco RI; 1st
strand CDNA was primed with a Not I - oligo(dT) primer [5,
TGTTACCATCTGAGTGGCGCGCCGATTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M.Fatima Bonaldo. RNA was kindly provided by
Dr. Minoru Ko (Wayne State University)."
113 a 112 c 118 g 87 t

[illegible]

Query Match 68.7%; Score 15.8; DB 27; Length 430;
Best Local Similarity 63.6%; Pred. No. 1.2e+02;
Matches 14; Conservative 4; Mismatches 4; Indels 0

QY 2 cngtngartggaaayttygcnmng 23
| | | | | : | | | | | : | |
Db 371 CACTTGAGGGGAACTTTGCCAG 392

Search completed: October 1, 1999, 15:03:38
Job time: 4382 sec
